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**In the Specification:**

*Change 1: Please insert the following seven paragraphs into the specification at page3, line 26 as follows:*

**BRIEF DESCRIPTION OF THE DRAWINGS**

Figures 1A-1E show consecutive segments of sequence alignment for two BASB029 polynucleotides, SEQ ID NO:1 and 3.

Figures 2A-2B show consecutive segments of sequence alignment for two BASB029 polypeptides, SEQ ID NO:2 and 4.

Figure 3 shows expression and purification of recombinant BASB029 in E. coli. A substantially purified BASB029 protein fraction (more than 80%) was separated on a 4-20% gradient polyacrylamide gel (NOVEX) under PAGE-SDS conditions in parallel to a protein molecular weight marker. Gels were either stained with Coomassie Blue R250 (lane 1) or analyzed by western blot using an anti-(His5) monoclonal antibody (lane 2).

Figure 4 shows recognition of the BASB029 protein on several NmB strains with BASB029 immunized mice sera.

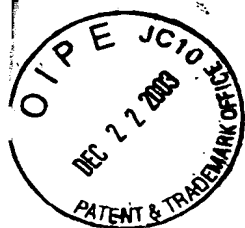
Figure 5 shows recognition of the BASB029 protein on several NmB strains with BASB029 immunized mice sera.

Figure 6 shows anti-BASB029 antibodies in convalescent sera (part B) and in immunized mice (part A).

Figure 7 shows anti-BASB029 antibodies in convalescent sera (part B) and in immunized mice (part A).

*Change 2: Please insert the following paragraph at page 57, line 2:*

What is claimed is:



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**Figure 1A**

**Identity to SeqID No:1 is indicated by a dot, and a dash ("-") indicates a missing nucleotide.**

```

                *      20      *      40      *
Seqid1 : ATGAACAAAATATACCGCATCATTTGGAATAGTGCCCTCAATGCCTGGGT : 50
Seqid3 : ..... : 50

                60      *      80      *      100
Seqid1 : CGCCGTATCCGAGCTCACACGCAACCACACCAAACGCGCTCCGCAACCG : 100
Seqid3 : ..... : 100

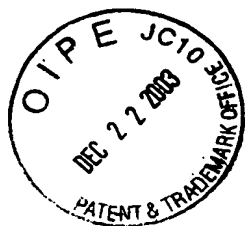
                *      120      *      140      *
Seqid1 : TGGCGACCGCGTATTGGCGACACTGTTGTTTGCAACGGTTCAGGCGAGT : 150
Seqid3 : ..AA.....A... : 150

                160      *      180      *      200
Seqid1 : ACTACCGAT-----GACGACGATTTATATTTAGAACCCGTACAACG : 191
Seqid3 : G...A.A..GAAGAGCAA..A..A.....C..... : 200

                *      220      *      240      *
Seqid1 : CACTGCTGTCGTGTTGAGCTTCCGTTCCGATAAAGAAGGCACGGGAGAAA : 241
Seqid3 : .....T..C.....TAG..AA..... : 250

                260      *      280      *      300
Seqid1 : AAG---AAGTTACAGAAGATTCAAATTGGGGAGTATATTTGACAAGAAA : 288
Seqid3 : ...AAA....AGA....A....G.....C.....A..G..... : 300

                *      320      *      340      *
Seqid1 : GGAGTACTAACAGCCGGAACAATCACCTCAAAGCCGGCGACAACCTGAA : 338
Seqid3 : .....A..GA..... : 350
```



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**Figur 1B**

```

          360          *          380          *          400
Seqid1 : AATCAAACAAAACACCAATGAAAACACCAATGCCAGTAGCTTCACCTACT : 388
Seqid3 : .....-----G..CA.A..... : 382

          *          420          *          440          *
Seqid1 : CGCTGAAAAAAGACCTCACAGATCTGACCAGTGTGGAACTGAAAAATTA : 438
Seqid3 : ..... : 432

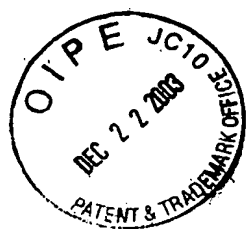
          460          *          480          *          500
Seqid1 : TCGTTTAGCGCAAACAGCAATAAAGTCAACATCACAAGCGACACCAAAGG : 488
Seqid3 : .....G..... : 482

          *          520          *          540          *
Seqid1 : CTTGAATTTTCGCGAAAAAACGGCTGAGACCAACGGCGACACCACGGTTC : 538
Seqid3 : .....T.....G.....G...G..... : 532

          560          *          580          *          600
Seqid1 : ATCTGAACGGTATCGGTTCGACTTTGACCGATACGCTGCTGAATACCGGA : 588
Seqid3 : .C.....T..... : 582

          *          620          *          640          *
Seqid1 : GCGACCACAAACGTAACCAACGACAACGTTACCGATGACGAGAAAAAACG : 638
Seqid3 : ..... : 632

          660          *          680          *          700
Seqid1 : TGCGGCAAGCGTTAAAGACGTATTAAACGCAGGCTGGAACATTAAAGGCG : 688
Seqid3 : ..... : 682
```



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**Figure 1C**

```

          *           720           *           740           *
Seqid1 : TTAAACCCGGTACAACAGCTTCCGATAACGTTGATTTCGTCCGCACTTAC : 738
Seqid3 : ..... : 732

          760           *           780           *           800
Seqid1 : GACACAGTCGAGTTCTTGAGCGCAGATACGAAAACAACGACTGTTAATGT : 788
Seqid3 : ..... : 782

          *           820           *           840           *
Seqid1 : GGAAAGCAAAGACAACGGCAAGAGAACCGAAGTTAAAATCGGTGCGAAGA : 838
Seqid3 : .....A..... : 832

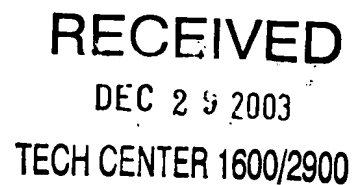
          860           *           880           *           900
Seqid1 : CTTCTGTTATCAAAGAAAAAGACGGTAAGTTGGTTACTGGTAAAGACAAA : 888
Seqid3 : .....T..... : 882

          *           920           *           940           *
Seqid1 : GGCGAGAATGATTCTTCTACAGACAAAGGCGAAGGCTTAGTGACTGCAAA : 938
Seqid3 : .....G.....G..... : 932

          960           *           980           *           1000
Seqid1 : AGAAGTGATTGATGCAGTAAACAAGGCTGGTTGGAGAATGAAAACAACAA : 988
Seqid3 : ..... : 982

          *           1020           *           1040           *
Seqid1 : CCGCTAATGGTCAAACAGGTCAAGCTGACAAGTTTGAAACCGTTACATCA : 1038
Seqid3 : ..... : 1032

          1060           *           1080           *           1100
Seqid1 : GGCACAAATGTAACTTTGCTAGTGGTAAAGGTACAACGCGACTGTAAG : 1088
Seqid3 : ..... : 1082
```

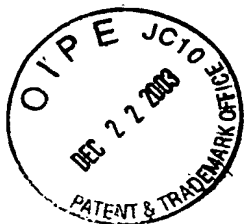


### Figure 1D

```

          *          1420          *          1440          *
Seqid1  : AAGCGTGGATGACGAGGGCGCGTTGAATGTCTGGCAGCAAGGATGCCAACA : 1438
Seqid3  : G.....---.G..A...A.....A.G.A.... : 1429

```



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**Figure 1E**

1460 \* 1480 \* 1500  
Seqid1 : AACCCGTCCGCATTACCAATGTCGCCCCGGGCGTTAAAGAGGGGGATGTT : 1488  
Seqid3 : ..... : 1479

\* 1520 \* 1540 \*  
Seqid1 : ACAAACGTCGCACAACCTTAAAGGCGTGGCGCAAACTTGAACAACCACAT : 1538  
Seqid3 : .....G... : 1529

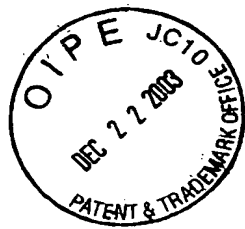
1560 \* 1580 \* 1600 \*  
Seqid1 : CGACAATGTGGACGGCAACGCGCGTGC GGCGCATCGCCCAAGCGATTGCAA : 1588  
Seqid3 : ..... : 1579

\* 1620 \* 1640 \*  
Seqid1 : CCGCAGGTCTGGTTCAGGCGTATCTGCCGGCAAGAGTATGATGGCGATC : 1638  
Seqid3 : .....T..... : 1629

1660 \* 1680 \* 1700  
Seqid1 : GGCGGCGGCACTTATCGCGGCGAAGCCGGTTATGCCATCGGCTACTCAAG : 1688  
Seqid3 : .....C.....C.. : 1679

\* 1720 \* 1740 \*  
Seqid1 : CATTTCCGACGGCGGAAATTGGATTATCAAAGGCACGGCTTCCGGCAATT : 1738  
Seqid3 : T..... : 1729

1760 \* 1780 \*  
Seqid1 : CGCGCGGCCATTTTCGGTGCTTCCGCATCTGTCGGTTATCAGTGGTAA : 1785  
Seqid3 : ..... : 1776



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Figure 2A

Identity to SeqID No:2 is indicated by a dot, and a dash ("-") indicates a missing amino acid.

```
          *          20          *          40          *
Seqid2 : MNKIYRIIWN SALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQAS : 50
Seqid4 : .....K..... : 50
```

```
          60          *          80          *          100
Seqid2 : T---TDDDDLYLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKK : 96
Seqid4 : ANNEEQEE....D....VA..IVN.....K.E.....A....E. : 100
```

```
          *          120          *          140          *
Seqid2 : GVLTAGTITLKAGDNLKIKQNTNENTNASSFTYSLKKDLTDLTSVGTEKL : 146
Seqid4 : .....RE.....-----G.N..... : 144
```

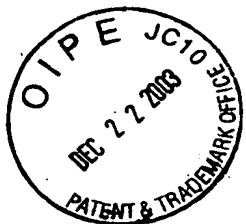
```
          160          *          180          *          200
Seqid2 : SFSANSNKVNITS DTKGLNFAKKTAE TNGD TTVHLNGIGSTLTDTLLNTG : 196
Seqid4 : .....G.....E..G..... : 194
```

```
          *          220          *          240          *
Seqid2 : ATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTY : 246
Seqid4 : ..... : 244
```

```
          260          *          280          *          300
Seqid2 : DTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGLVTGKDK : 296
Seqid4 : ..... : 294
```

```
          *          320          *          340          *
Seqid2 : GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKT T T TANGQTGQADKFETVTS : 346
Seqid4 : ...G....E..... : 344
```





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**Figure 2B**

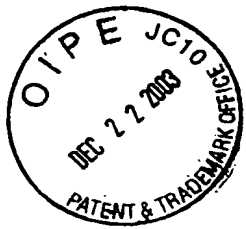
360 \* 380 \* 400  
Seqid2 : GTNVTFASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLD : 396  
Seqid4 : ..... : 394

\* 420 \* 440 \*  
Seqid2 : KAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMT : 446  
Seqid4 : ..... : 444

460 \* 480 \* 500  
Seqid2 : PQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDV : 496  
Seqid4 : .....GD-.....KD..... : 493

\* 520 \* 540 \*  
Seqid2 : TNVAQLKGVAQNLNNHIDNV DGNARAGIAQAIATAGLVQAYLPGKSMMAI : 546  
Seqid4 : .....R..... : 543

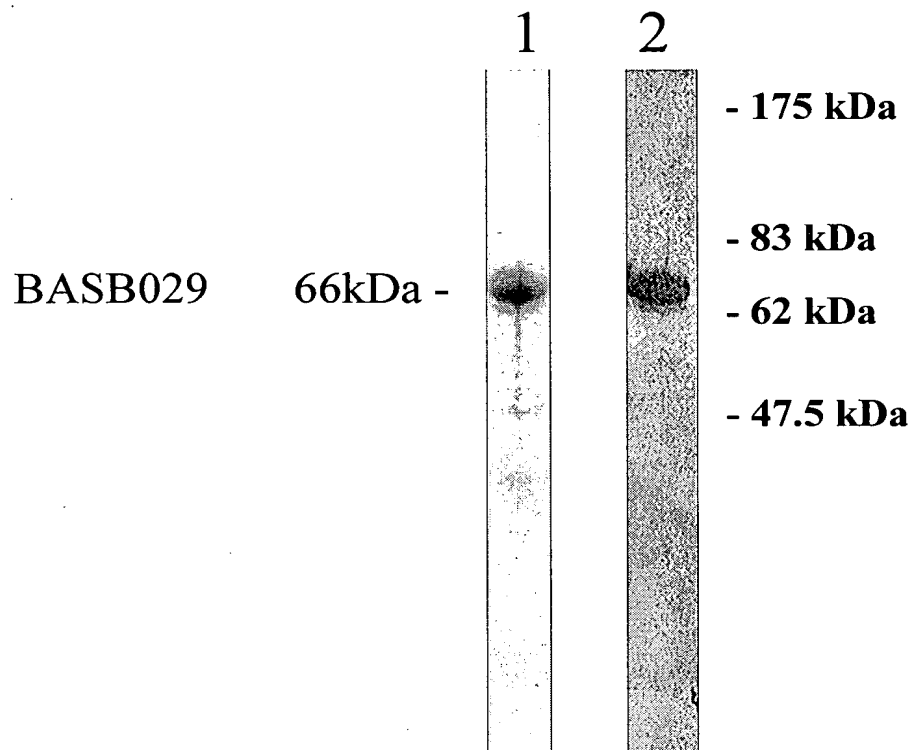
560 \* 580 \*  
Seqid2 : GGGTYRGEAGYAIGYSSISDGGNWI IKG TASGNSRGHFGASASVGYQW : 594  
Seqid4 : ..... : 591



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**Figure 3**

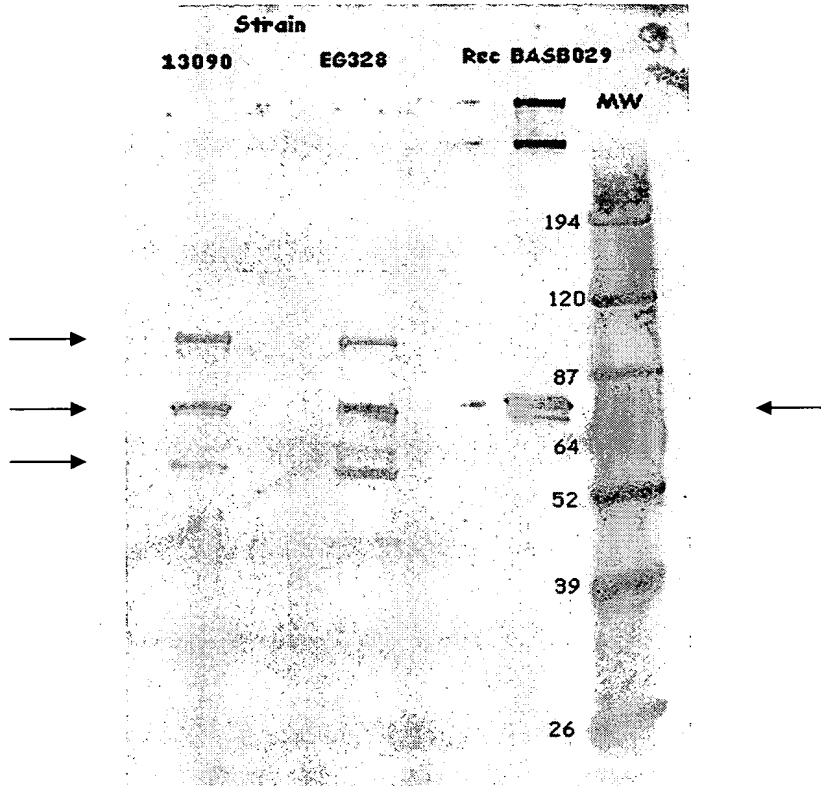


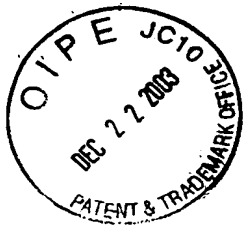


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**Figure 4**

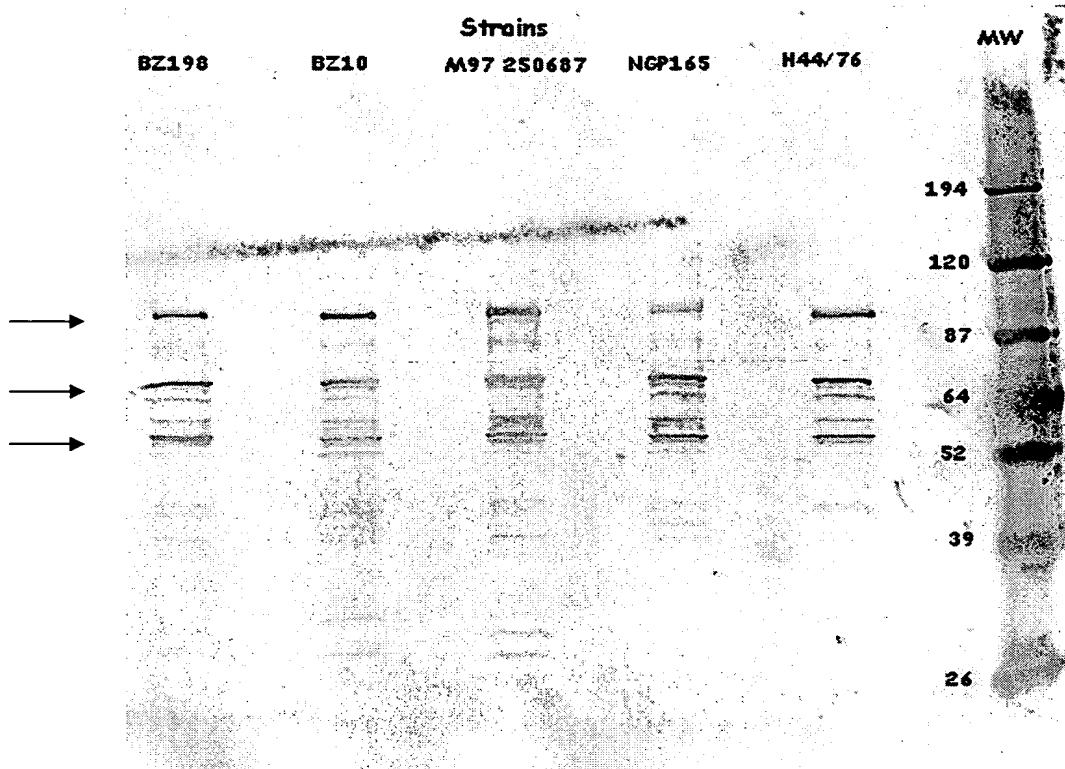


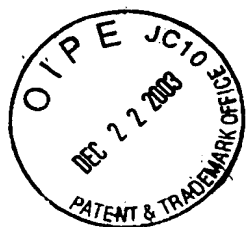


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**Figure 5**

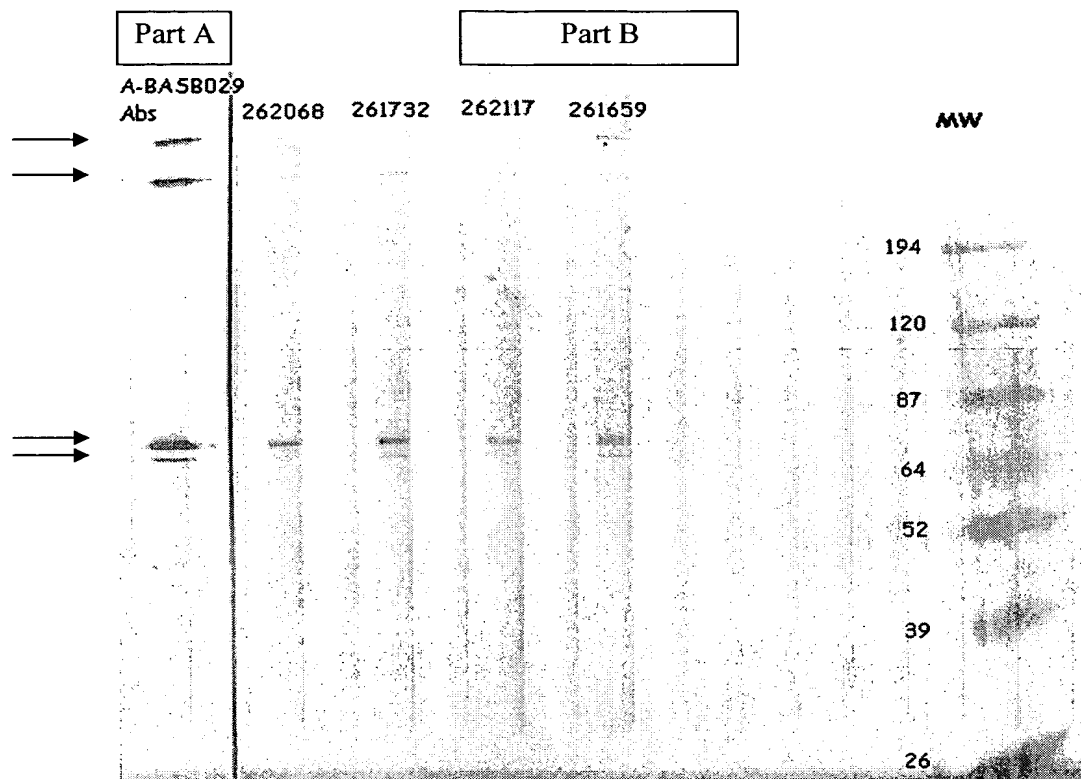


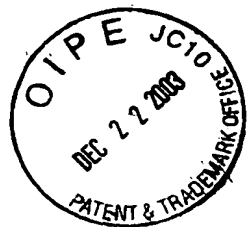


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Figure 6





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Figure 7

